AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application.

1.-85. (Canceled)

86. (Currently Amended) A method for detecting the taxonomic unit of enterobacteria ~~bacteria~~ in an analytical sample, comprising the step of bringing the analytical sample into contact with an added nucleic acid or a combination of added nucleic acids, and detecting suitable hybrid nucleic acids comprising at least one of the added nucleic ~~acid~~ acids and bacterial nucleic acid, wherein the one or more added nucleic acids are selected from the group consisting of:

a) nucleic acid molecules comprising at least one sequence ~~with any~~ of SEQ ID NOs: 2 and 78 ~~1 to 530 and/or a sequence from position 2667 to 2720, 2727 to 2776, 2777 to 2801, 2801 to 2832, 2857 to 2896, 2907 to 2931, 2983 to 2999 and/or 3000 to 3032 according to SEQ ID NO: 1; or nucleic acids which are homologous or at least 70% identical with them~~;

b) nucleic acid molecules which hybridize specifically with SEQ ID NO: 2 or 78 ~~a nucleic acid according to a)~~;

c) nucleic acid molecules which exhibit at least 70% identity with a nucleic acid according to a) ~~or b)~~; and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

87. (Canceled)

88. (Currently Amended) The method of claim 86, wherein the ~~process~~ method involves a PCR amplification of the bacterial nucleic acid ~~to be detected~~.

89. (Currently Amended) The method of claim 86, wherein the ~~process~~ method involves a Southern Blot hybridization.

90. - 91. (Canceled)

92. (Currently Amended) A method for amplifying bacterial DNA of a multiplicity of different taxonomic units, ~~especially genera and species, using primers, in which in~~ comprising a first amplification step in which the DNA for a ~~high~~ taxonomic ~~units such as classes, phyla or families~~ unit of the enterobacteria family is amplified with conserved primers to obtain a first amplification fragment, and, optionally, ~~in~~ at least one further amplification step (EN) in which parts of the first amplification fragment, which are specific for genera or species of the taxonomic unit, ~~can be~~ are multiplied with nested, increasingly variable primers, and, optionally, ~~in~~ a further step in which the DNA fragments obtained by amplification, which are specific for genera or species of the taxonomic unit, are detected by means of probes, wherein the primers used in the first amplification step comprise a nucleic ~~acids~~ acid selected from the group consisting of:

a) nucleic acid molecules comprising at least one sequence ~~with any~~ of the SEQ ID NOs: 2 and 78 ~~1 to 530 and/or a sequence from position 2667 to 2720, 2727 to 2776, 2777 to 2801, 2801 to 2832, 2857 to 2896, 2907 to 2931, 2983 to 2999 and/or 3000 to 3032 according to SEQ ID NO: 1, or nucleic acids which are homologous or at least 70% identical with them~~;

b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit at least 70% identity with a nucleic acid according to a) ~~or b)~~; and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

93. (Currently Amended) The method of claim 92, wherein the ~~process~~ method involves a PCR amplification of the bacterial nucleic acid ~~to be detected~~.

94. (Currently Amended) A method according to claim ~~Claim~~ 92, wherein the ~~process~~ method involves a Southern Blot hybridization.

95. (Canceled)

96. (Currently Amended) The method of claim 86, wherein ~~the~~ a nucleic acid molecule according to ~~alternative~~ c) exhibits at least 90% identity with a nucleic acid according to a) ~~or b)~~.

97. (Currently Amended) The method of claim 86, wherein the one or more added nucleic acid ~~molecule is~~ molecules are modified or labeled so that ~~it~~ they can generate a signal ~~in~~ for analytical detection ~~procedures which are known per se~~, with the modification or labeling selected from the group consisting of (i) radioactive groups, (ii) colored groups, (iii) fluorescent groups, (iv) groups for immobilization of a solid phase, and (v) groups which allow a direct or indirect reaction~~, especially using antibodies, antigens, enzymes, and/or substances with affinity to enzymes or enzyme complexes~~.

98. - 99. (Canceled)

100. (Currently Amended) A method for detecting bacteria having a bacterial nucleic acid in an analytical sample, comprising the step of bringing the analytical sample into contact with a combination of nucleic acids, and detecting suitable hybrid nucleic acids comprising one or more of the contacted nucleic acids and the bacterial nucleic acid, wherein the combination of nucleic acids comprises a combination of at least two nucleic acid molecules selected from the group consisting of ~~The method of claim 90, characterized in that the combination comprises at least one nucleic acid molecule selected from the group consisting of~~:

a) nucleic acid molecules comprising at least one sequence ~~with~~ of ~~any of the~~ SEQ ID NOs: 2 and 78 ~~25~~;

b) nucleic acid molecules which hybridize specifically with ~~a nucleic acid according to a)~~ any of SEQ ID NOs: 2 and 78;

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) ~~or b)~~; and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

101. (Canceled)

102. (Currently Amended) The method of claim 92, wherein the nucleic acid molecule according to ~~alternative~~ c) exhibits at least 90% identity with a nucleic acid according to a) ~~or b)~~.

103. - 104. (Canceled)

105. (Currently Amended) A method for amplifying bacterial DNA of a multiplicity of different taxonomic units, comprising a first amplification step in which the DNA for the taxonomic units of an enterobacteria family is amplified with conserved primers to obtain a first amplification fragment, and, optionally, at least one further amplification step (EN) in which parts of the first amplification fragment, which are specific for genera or species of the taxonomic unit, are multiplied with nested, increasingly variable primers, and optionally, a further step in which the DNA fragments obtained by amplification, which are specific for genera or species of the taxonomic unit, are detected by means of probes, wherein the primers used in the first amplification step comprise a combination of at least two nucleic acid molecules, selected from the group consisting of ~~The method of claim 95, wherein the primers used comprise at least one nucleic acid molecule selected from the group consisting of~~:

a) a combination of a nucleic acid molecule ~~molecules~~ comprising ~~at least one sequence with any of the~~ SEQ ID NOs: 2 ~~and~~ with a nucleic acid molecule comprising SEQ ID NO: 78 ~~25~~;

b) a combination of a nucleic acid molecule ~~molecules~~ which hybridizes ~~hybridize~~ specifically with ~~a nucleic acid according to a)~~ SEQ ID NO: 2, with a nucleic acid that hybridizes specifically with SEQ ID NO: 78;

c) a combination of a nucleic acid molecule ~~molecules~~ of a nucleic acid which exhibits ~~exhibit~~ 70% identity with ~~a nucleic acid according to a) or b); and~~ SEQ ID NO: 2, with a nucleic acid which exhibits 70% identity with SEQ ID NO: 78, and;

d) a combination of a nucleic acid molecules ~~which are complementary to a nucleic acid according to any of a) to c)~~ which are complementary to the combinations of a) to c).

106. (Canceled)

107. (New) The method of claim 97, wherein the groups which allow a direct or indirect reaction are selected from the group consisting of antibodies, antigens, enzymes, and substances with affinity to enzymes or enzyme complexes.